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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=12; hr=16; min=29; sec=19; ms=664;]

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Application No: 10808758 Version No: 3.0

Input Set:**Output Set:**

Started: 2008-02-27 21:36:38.302
Finished: 2008-02-27 21:36:44.860
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 558 ms
Total Warnings: 119
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-02-27 21:36:38.302
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Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 558 ms
Total Warnings: 119
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)
W 402	Undefined organism found in <213> in SEQ ID (39)
W 402	Undefined organism found in <213> in SEQ ID (40)

SEQUENCE LISTING

<110> The Scripps Research Institute
Von Seggern, Daniel J.

<120> ADENOVIRUS PARTICLES WITH ENHANCED INFECTIVITY OF DENDRITIC
CELLS AND PARTICLES WITH DECREASED INFECTIVITY OF HEPATOCYTES

<130> SCRIP1860-2

<140> 10808758

<141> 2004-03-24

<150> US 60/467,500

<151> 2003-05-01

<150> US 60/459,000

<151> 2003-03-28

<160> 122

<170> FastSEQ for Windows Version 4.0

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<211> 1746

<212> DNA

<213> Adenovirus type 5

<220>

<221> CDS

<222> (1)...(1743)

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tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc	96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
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ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct	144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc	192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	

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Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
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act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
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gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	
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Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
165 170 175	
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Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag	864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	
275 280 285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
305 310 315 320	

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
325 330 335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
340 345 350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
355 360 365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac	1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp	
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Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	
405 410 415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile	
420 425 430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata	1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile	
435 440 445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn	
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gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt	1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe	
465 470 475 480	
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Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly	
485 490 495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	
500 505 510	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa	1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	
515 520 525	
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac	1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	
530 535 540	
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 <212> PRT
 <213> Adenovirus type 5

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 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305		310		315		320
Val	Asn	Leu	Ser	Thr	Ala	Ile
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Ala	Ile	Asn	Ala	Gly	Asp	Pro
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Asn	Thr	Asn	Pro	Leu	Lys	Thr
		355		360		365
Ser	Asn	Lys	Ala	Met	Val	Pro
		370		375		380
Ser	Thr	Gly	Ala	Ile	Thr	Val
		385		390		395
Leu	Trp	Thr	Thr	Pro	Ala	Pro
				405		410
Lys	Asp	Ala	Lys	Leu	Thr	Leu
		420		425		430
Leu	Ala	Thr	Val	Ser	Val	Leu
		435		440		445
Ser	Gly	Thr	Val	Gln	Ser	Ala
		450		455		460
Gly	Val	Leu	Leu	Asn	Asn	Ser
		465		470		475
Arg	Asn	Gly	Asp	Leu	Thr	Glu
		485		490		495
Phe	Met	Pro	Asn	Leu	Ser	Ala
		500		505		510
Lys	Ser	Asn	Ile	Val	Ser	Gln
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Pro	Val	Thr	Leu	Thr	Ile	Thr
		530		535		540
Thr	Thr	Pro	Ser	Ala	Tyr	Ser
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Tyr	Ile	Ala	Gln	Glu		
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<220>
 <223> Synthetic construct: 5F KO1

<220>
 <221> CDS
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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
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tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc	96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct	144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc	192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
165 170 175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
210 215 220	
ggg cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	
245 250 255	

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	
260 265 270	
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Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	
275 280 285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
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Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
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gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
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gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1056
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Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp	
370 375 380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr	
385 390 395 400	
ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag	1248
Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu	
405	